

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 7, 2002, 15:40:21 ; Search time 180.87 Seconds
(without alignments)
499.786 Million cell updates/sec

Title: US-08-569-749-2

Perfect score: 3277

Sequence: 1 MHKTASQSLFPGPSQYONIKS.....LRKPCICRGIIKGVTRFLS 618

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL_17:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2630	80.3	589	11 Q9QZC6	Q9qz6 ratius nov
2	2625	80.1	589	11 Q9SESE8	Q9ses8 ratius nov
3	2339	71.4	610	13 Q57319	Q57319 gallus gall
4	2185	66.7	602	11 Q9SESE9	Q9ses9 ratius nov
5	1678	51.2	1140	4 Q9UNH1	Q9unh1 homo sapien
6	1138.5	34.7	324	13 Q9PDN2	Q9pdn2 gallus gall
7	945.5	28.9	224	11 Q8642	Q8642 ratius nov
8	898.5	27.4	501	11 Q9EQ05	Q9eq05 ratius nov
9	898.5	27.4	501	11 Q9EQ04	Q9eq04 ratius nov
10	896.5	27.4	496	11 Q9SEF0	Q9sef0 ratius nov
11	801.5	24.5	197	13 Q9IA69	Q9ia69 gallus gall
12	796.5	24.3	195	13 Q9IA70	Q9ia70 gallus gall
13	494	15.1	597	11 Q9H015	Q9h015 mus musculu
14	490	15.0	438	5 Q9VUX5	Q9vux5 drosophila
15	486	14.8	281	12 Q9YNL8	Q9ynl8 choristoneu
16	481.5	14.7	379	5 Q9U492	Q9u492 trichoplusi
17	476	14.5	264	12 Q9EN27	Q9en27 ansacta moo
18	475.5	14.5	276	12 Q89744	Q89744 buzzura supp
19	470	14.3	261	12 Q9QES9	Q9qes9 epiphyas po

20	466.5	14.2	377	5 Q9N107	Q9n107 spodoptera
21	462.5	14.1	280	4 Q9HAP7	Q9hap7 homo sapien
22	460.5	14.1	298	4 Q9H2A8	Q9h2a8 homo sapien
23	423.5	12.9	313	12 Q9J827	Q9j827 spodoptera
24	368.5	11.2	268	12 Q9IP18	Q9ip18 helicoverpa
25	363.5	11.1	268	12 Q9E232	Q9e232 helicoverpa
26	287	8.8	80	4 Q9HC27	Q9hc27 homo sapien
27	240	7.3	292	12 Q9C394	Q9c394 bombyx mori
28	239.5	7.3	210	4 Q9B0V0	Q9bv0 homo sapien
29	231.5	7.1	284	12 Q9YKL5	Q9ykl5 epiphyas po
30	222	6.8	285	12 Q9PYQ9	Q9pyq9 xestlia c-n1
31	220	6.7	301	12 Q9P254	Q9p254 trichoplusi
32	194	5.9	4845	11 Q88738	Q88738 mus musculu
33	186.5	5.7	316	5 Q44624	Q44624 caenorhabdi
34	182	5.6	281	12 Q9DVT5	Q9dvt5 pluteella xy
35	181.5	5.5	711	10 Q82304	Q82304 arabidopsis
36	175.5	5.4	208	12 Q55770	Q55770 chilo iride
37	173.5	5.3	317	12 Q9J849	Q9j849 spodoptera
38	169	5.2	150	12 Q9YVJ4	Q9yv4 melanoplus
39	168.5	5.1	187	12 Q9DSM8	Q9dsw8 ascovirus d
40	168	5.1	445	4 Q9HHE7	Q9hhe7 homo sapien
41	168	5.1	445	4 Q9BU73	Q9bu73 homo sapien
42	167	5.1	372	4 Q9H6W8	Q9h6w8 homo sapien
43	165	5.0	376	11 Q9GKR6	Q9gkr6 mus musculu
44	164	5.0	4904	5 Q9VH01	Q9vh01 drosophila
45	161	4.9	155	12 Q9YMI9	Q9ymi9 lymantria d

ALIGNMENTS

RESULT 1
Q9QZC6 PRELIMINARY: PRT: 589 AA.
AC Q9QZC6: 01-MAY-2000 (TREMBLrel, 13, Created)
DT 01-MAY-2000 (TREMBLrel, 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel, 17, Last annotation update)
DE INHIBITOR OF APOPTOSIS PROTEIN 2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP TISSUE=KIDNEY.
RC DONG Z., Denton M., Gu S.M., Saikumar P., Venkatachalam M.A.;
RT "Cloning of cDNA for rat inhibitor of apoptosis protein 2."
RT Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.
DR EMBL: AF190020; AAF04585.1; -.
DR HSSP: O13490; 10BH.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; Znf_fing.
DR Pfam: PF00653; BIR; 3.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 3.
DR PROSITE: PS0143; BIR_REPEAT_2; 3.
DR PROSITE: PS0209; CARD; 1.
KW Zinc-finger.
SQ SEQUENCE 589 AA: 66777 MW: E6812PFE3EA34142 CRC64;

Query Match 80.3%; Score 2630; DB 11; Length 589;
Best Local Similarity 81.7%; Pred. No. 1.3e-177;
Matches 488; Conservative 53; Mismatches 48; Indels 8; Caps 4;
QY 22 MEDSTILSWTNSKQKKYDPCSLYKMSITYSTPACVPSERSLACAGYYTCVNDKV 81

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DB 1 MENSTVLSNMWTKENKEMKYDFSCELYRMSTYSAPFRGVPVSESLARAGFYTTGVNDKV 60
OY 82 KCFCGGLMDNMKKLDGSPYIOKHOLYPSCSFIONIVSASLGSKTSKMRNSFAHSLSP 141
DB 61 KCFCGGLMDNMKKLDGSPYIOKHOLYPSCSFIONIVSASLGSKTSKMRNSFAHSLSP 118
OY 142 TLEHSSLSFGSYSSLPNLSRAVEDISSRTPNYSYAMSTEARFLTYHMMPLTFLSP 201
DB 119 PLEQ----GGHSSLPSPNLSRAVEDF--SLMNPCTYAMSTEARFLTYHMMPLTFLSP 173
OY 202 SELARAGFYITGPDRAVACFACGKLSNMEPKDDAMSEHRRHPNCPLENSLETLRFSI 261
DB 174 AELAKAGFYITGPDRAVACFACGKLSNMEPKDDAMSEHRRHPNCPLENSLETLRFSV 233
OY 262 SNLSQTHAARMRTFMYVPSVPVOPDOLASAGFYVGNDDVKCCDGLRCMESGDD 321
DB 234 SNLSQTHAARMRTFMYVPSVPVOPDOLASAGFYVGNDDVKCCDGLRCMESGDD 293
OY 322 PVEHAKNFPCEFLIRKKGOFVDEIOGRYPHLLLEQLSTSDTTEENADPPIIHFGPG 381
DB 294 PVEHAKNFPCEFLIRKKGOFVDEIOGRYPHLLLEQLSTSDTSEENADPPIVHFGPG 353
OY 382 ESSSEDAVMNTPPVYKSALEMGNRDLYVQVOSKLTGTGENYKTVNDIVSALLNAEDEK 441
DB 354 E-NMEDAVAMNTPPVYKSALEMGNRDLYVQVOSKLTGTGENYKTVNDIVSALLNAEDEK 412
OY 442 REEEKKAEEMASDLSLIRKNRMALFOOLTCVPIIDNLLKANVINKEHDIIRKQTO 501
DB 413 REEEKKAEEMASDLSLIRKNRMALFOOLTCVPIIDNLLKANVINKEHDIIRKQTO 472
OY 502 IPLQARELIDTILVKGNAAMAFKNCLEKIDSTLYKNLFVDKNMKYIPTEDVSGLSLEQ 561
DB 473 IPLQARELIDTILVKGNAAMAFKNCLEKIDSTLYKNLFVDKNMKYIPTEDVSGLSLEQ 532
OY 562 LRRLOEERTCKVCMDEKESVIFPCGHLVVCQECAPSLKRCPIKGIITGVTRFPLS 618
DB 533 LRRLOEERTCKVCMDEKESVIFPCGHLVVCQECAPSLKRCPIKGIITGVTRFPLS 589

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SQ SEQUENCE 589 AA; 66750 MW; B4F7089BD7CD285B CRC64;
Query Match 80.1%; Score 2625; DB 11; Length 589;
Best Local Similarity 81.6%; Pred. No. 2.9e-177;
Matches 487; Conservative 54; Mismatches 48; Indels 8; Gaps 4;
OY 22 MEDSTILSDWTNNSNKKKKYDFSCELYRMSTYSAPFRGVPVSESLARAGFYTTGVNDKV 81
DB 1 MENSTVLSNMWTKENKEMKYDFSCELYRMSTYSAPFRGVPVSESLARAGFYTTGVNDKV 60
OY 82 KCFCGGLMDNMKKLDGSPYIOKHOLYPSCSFIONIVSASLGSKTSKMRNSFAHSLSP 141
DB 61 KCFCGGLMDNMKKLDGSPYIOKHOLYPSCSFIONIVSASLGSKTSKMRNSFAHSLSP 118
OY 142 TLEHSSLSFGSYSSLPNLSRAVEDISSRTPNYSYAMSTEARFLTYHMMPLTFLSP 201
DB 119 PLEQ----GGHSSLPSPNLSRAVEDF--SLMNPCTYAMSTEARFLTYHMMPLTFLSP 173
OY 202 SELARAGFYITGPDRAVACFACGKLSNMEPKDDAMSEHRRHPNCPLENSLETLRFSI 261
DB 174 AELAKAGFYITGPDRAVACFACGKLSNMEPKDDAMSEHRRHPNCPLENSLETLRFSV 233
OY 262 SNLSQTHAARMRTFMYVPSVPVOPDOLASAGFYVGNDDVKCCDGLRCMESGDD 321
DB 234 SNLSQTHAARMRTFMYVPSVPVOPDOLASAGFYVGNDDVKCCDGLRCMESGDD 293
OY 322 PVEHAKNFPCEFLIRKKGOFVDEIOGRYPHLLLEQLSTSDTTEENADPPIIHFGPG 381
DB 294 PVEHAKNFPCEFLIRKKGOFVDEIOGRYPHLLLEQLSTSDTSEENADPPIVHFGPG 353
OY 382 ESSSEDAVMNTPPVYKSALEMGNRDLYVQVOSKLTGTGENYKTVNDIVSALLNAEDEK 441
DB 354 E-NMEDAVAMNTPPVYKSALEMGNRDLYVQVOSKLTGTGENYKTVNDIVSALLNAEDEK 412
OY 442 REEEKKAEEMASDLSLIRKNRMALFOOLTCVPIIDNLLKANVINKEHDIIRKQTO 501
DB 413 REEEKKAEEMASDLSLIRKNRMALFOOLTCVPIIDNLLKANVINKEHDIIRKQTO 472
OY 502 IPLQARELIDTILVKGNAAMAFKNCLEKIDSTLYKNLFVDKNMKYIPTEDVSGLSLEQ 561
DB 473 IPLQARELIDTILVKGNAAMAFKNCLEKIDSTLYKNLFVDKNMKYIPTEDVSGLSLEQ 532
OY 562 LRRLOEERTCKVCMDEKESVIFPCGHLVVCQECAPSLKRCPIKGIITGVTRFPLS 618
DB 533 LRRLOEERTCKVCMDEKESVIFPCGHLVVCQECAPSLKRCPIKGIITGVTRFPLS 589

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RESULT 2
OQESB8 PRELIMINARY; PRT; 589 AA.
AC OQESB8;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE INHIBITOR OF APOPTOSIS PROTEIN 2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN (1)
RP SEQUENCE FROM N.A.
RA Holcik M., Lefebvre C.A., Hicks K., Korneluk R.G.;
RT "Cloning and Characterization of the Rat Homologs of the Inhibitor of
RT Apoptosis Protein 1, 2, and 3 Genes."
RT Submitted (SEP-1999) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.
DR EMBL: AF163431; AAC22971.1; -.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR pfam: PF00653; BIR; 3.
DR pfam: PF00619; CARD; 1.
DR pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 1.
DR PROSITE: PS0143; BIR_REPEAT_2; 3.
DR PROSITE: PS0209; CARD; 1.
KW Zinc-finger.

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RESULT 3
O57319 PRELIMINARY; PRT; 610 AA.
AC O57319;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE INHIBITOR OF APOPTOSIS PROTEIN 1 (IAP) (INHIBITOR OF T CELL APOPTOSIS
DE PROTEIN).
GN IAP1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_Taxid=9031;
RN (1)
RP SEQUENCE FROM N.A.
RA STRAIN-WHITE LEHORN; TISSUE-EMBRYONIC FIBROBLAST;
RE MEDLINE=9603801; Pubmed=9372964;
RA You M., Ku P.-T., Hrdlickova R., Bose H.R. Jr.;
RT "ch-IAP1, a member of the inhibitor-of-apoptosis protein family, is a
RT mediator of the antiapoptotic activity of the v-rel oncoprotein."
RT Mol. Cell. Biol. 17:7328-7341(1997).
CC -1- FUNCTION: SUPPRESSOR OF APOPTOSIS IN ONCOPROTEIN V-REL-TRANSFORMED
CC CELLS.

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CC -1- SUBCELLULAR LOCATION: EXPRESSED PREDOMINANTLY IN THE CYTOPLASM OF
CC THE V-REL-TRANSFORMED CELLS.
CC -1- TISSUE SPECIFICITY: EXPRESSED AT RELATIVELY HIGH LEVELS IN THE
CC SPLEEN, THYMUS, BURSAS, INTESTINE, AND LUNG, AND AT VERY LOW LEVELS
CC IN TESTIS, BRAIN, AND SKELETAL MUSCLE.
CC -1- INDUCTION: INDUCED DURING THE V-REL-MEDIATED TRANSFORMATION
CC PROCESS.
CC -1- DOMAIN: THE RING FINGER IS IMPORTANT FOR ITS ANTIAPOPTOTIC EFFECT.
CC -1- SIMILARITY: MEMBER OF THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR DOMAINS (BACULOVIRAL INHIBITION OF
CC APOPTOSIS PROTEIN REPEAT).
CC -1- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
CC EMBL: AF008592; AAB88044.1; -.
CC HSSP: Q13490; 10BH.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; ZnF_ring.
DR Pfam: PF00653; BIR; 3.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 3.
DR PROSITE: PS0143; BIR_REPEAT_2; 3.
DR PROSITE: PS50209; CARD; 1.
DR Apoptosis: Zinc-finger; Repeat.
KM REPEAT 30 97 BIR_REPEAT 1.
FT REPEAT 176 242 BIR_REPEAT 2.
FT REPEAT 262 329 BIR_REPEAT 3.
FT ZN_FING 563 597 C3HC4-TYPE.
SQ SEQUENCE 610 AA; 68924 MW; ADF47619650B44A6 CRC64;

Query Match 71.4%; Score 2339; DB 13; Length 610.
Best Local Similarity 71.4%; Pred. No. 4,7e-157;
Matches 437; Conservative 78; Mismatches 81; Indels 16; Gaps 7;

QY 20 SIMEDSTLSDMTNSNKO--KKMKYDFSCELYRMSTYTFPPAGVPYSESLARAGFYTCV 77
DB 2 NIMDSPLSLAVKQNAHOGELKYDLSCELYRMSTYTFPPVAVSERKLARAGFYTCV 61
QY 78 NDKVCFCCGLMDNMKLGDSPIQKHQOLYPCSCFIQNLVSA-SLG-ST-----SKN 127
DB 62 QDKVCFCCGLVDMNQPDGNAMKHKQYPCSCFQNNLSLNLGLSTHSAFSLVAVSN 121
QY 128 TSPMRKSFHSLSPTEHSLFSGYSLSLSPNLSRAVEDISSRTNPFYSTAMSTEER 187
DB 122 LSPSLRSM--TLSPSEQVGYFGSFSPPDPVYTRAEDLSHLSKSLHNSMSTEEAR 179
QY 188 FLTYHMPPLTFPSPELARAGFYIIGPDRVACFCGCKLSNMPEPDDAMSEHRRHFPNC 247
DB 180 LRFTHMPLMFLSPALAKAGLYLTGTAKVACFTCGGLSNMPEPDDAMSEHRRHFPNC 239
QY 248 PLELNSL-ETLRFISNLISMQTHAARMRTFMTWPSSVPVQPEOLASAGFYVYGRNDVYC 306
DB 240 PVEYNLMRQPSFNVSNVMTQTHEARVKTFTIMWPRIPVQPEOLADAGFYVYGRNDVYC 299
QY 307 FCCDGLRCMESGDDPWVHAHAKWPRCEFLIRKGOEFVDEIGRPHLLBOLLSTSDT 366
DB 300 FCCDGLRCMESGDDPWVHAHAKWPRCEFLIRKGOEFVDEIGRPHLLBOLLSTSDT 359
QY 367 GREENAPPLIHFGPESSESDAVMNTPVVKSALKEGFRNDLVKQTVOSKITLTTGENY 426
DB 360 VNDENMD-PIIHFGPESSEDATIMNTPVVKSALKEGFRNDLVKQTVOSKITLTTGENY 418
QY 427 VNDIVALLNAEDKEEREKEKQAEEMASDLSLRKNMALFOOLTCVPLTIDNLKAN 486
DB 419 VNDIVALLNAEDKEEREKEKQAEEMASDLSLRKNMALFOOLTCVPLTIDNLKAN 478
QY 487 VINKOHDIKOKTQPLQARELIDFLVKGNAANAFIFNCKLEIDSTLYKMLPYDKNKK 546
DB 479 VITELEHDIKOKTQPLQARELIDFLVKGNAANAFIFNCKLEIDSTLYKMLPYDKNKK 538
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QY 547 YTPEDVSGLSLEQRLRLQERTCKYCMDEKSVVTFPCGHLVYQECAPSLRKPICR 606
DB 539 YTPEDVSGLSLEQRLRLQERTCKYCMDEKSVVTFPCGHLVYQECAPSLRKPICR 598
QY 607 GIKGTAVTFELS 618
DB 599 GTIKGTAVTFELS 610

RESULT 4
Q9ESE9 PRELIMINARY; PRT: 602 AA.
ID Q9ESE9
AC Q9ESE9;
DT 01-MAR-2001 (Tremblrel, 16, Created)
DT 01-MAR-2001 (Tremblrel, 16, Last sequence update)
DT 01-JUN-2001 (Tremblrel, 17, Last annotation update)
DE INHIBITOR OF APOPTOSIS PROTEIN 1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Holcik M., Lefebvre C.A., Hicks K., Korneluk R.G.;
RT "Cloning and Characterization of the Rat Homologs of the Inhibitor of
RT Apoptosis Protein 1, 2, and 3 Genes."
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.
CC EMBL: AF183430; AAG22970.1; -.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; ZnF_ring.
DR Pfam: PF00653; BIR; 3.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 1.
DR PROSITE: PS0143; BIR_REPEAT_2; 3.
DR PROSITE: PS50209; CARD; 1.
KW Zinc-finger.
SQ SEQUENCE 602 AA; 67326 MW; CC91385BEA62DE5A CRC64;

Query Match 66.7%; Score 2185; DB 11; Length 602;
Best Local Similarity 67.4%; Pred. No. 3,4e-146;
Matches 411; Conservative 86; Mismatches 93; Indels 20; Gaps 7;

QY 20 SIMEDSTLSDMTNS--NKOKMKYDFSCELYRMSTYTFPPAGVPYSESLARAGFYTCV 78
DB 2 NIMDSAPLALKMSADDFELKIDFSCELYRUSTYTFPPAGVPYSESLARAGFYTCV 61
QY 79 DKVCFCCGLMDNMKLGDSPIQKHQOLYPCSCFIQNLVSA-----LGSTSNKTS 129
DB 62 DKVCFCCGLMDNMKLGDSPIQKHQOLYPCSCFIQNLVSA-----LGSTSNKTS 119
QY 130 PMRNSFAHSLSPTEHSLFSGYSLSLSPNLSRAVEDISSRTNPFYSTAMSTEER 189
DB 120 TMSPEFASL-----ESTYTFSGYSLSFSPSDPVNRAQDDCPAFSTSPYHRAAMNTEKARLL 174
QY 190 TYHMPPLTFPSPELARAGFYIIGPDRVACFCGCKLSNMPEPDDAMSEHRRHFPNC 249
DB 175 TYQWPLPSFLSPALAKAGFYITGPDVACFCGCKLSNMPEPDDAMSEHRRHFPNC 234
QY 250 LENSLIE-TLRFISNLISMQTHAARMRTFMTWPSSVPVQPEOLASAGFYVYGRNDVYC 308
DB 235 LKDVQGFYSQYTVSNLSMQTHAARMRTFMTWPSSVPVQPEOLASAGFYVYGHSDVAVCF 294
QY 309 CDGGLRCMESGDDPWVHAHAKWPRCEFLIRKGOEFVDEIGRPHLLBOLLSTSDTGE 368
DB 295 CDGGLRCMESGDDPWVHAHAKWPRCEFLIRKGOEFVQVQVAGYPHLLBOLLSTSDPED 354
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OY	369	ENAPPTIIHGPGSSSDVAMNMTPVKSAALMGFNPDIVKTQYSKLTTGENTKNV	428
Dd	355	ETGEAAIYHLAGPGE-WMEDAVMANTPVYKKAALDMGFSRSLVROTVOYRLLATGENTRTVS	413
OY	429	DIVSALLNADEBKEEKEERKEKOAEBSMDLSLRKRPMALFOOLTCTVLTLIDNLKANVI	488
Dd	414	DLVIGLILDAEDEMNEEDTBDGAEEBEESDDLTLLRKNNMYLLQHLPVPFTIIDCLLSARI	473
OY	489	NKOEHDIIKKOKTOPILOARELIDITLVKGNAAANFRNCLEIKDISTVLYKNLFVDNMKMYI	548
Dd	474	TEOEGDVAVKOPKPH-TLOARFLIDITVLAKGTNTATSFRNSHQETIDPELYRDIPVRONIRSL	532
OY	549	PTEBVSGLSLEEOURLROERTCKVCMDKRSVSVFIPCCHLVVCOCCASLKCPCICRI	608
Dd	533	PTDIIAALPHEEBOLRLQLBERTCKVCMDREASLVFPICPHLVVCKBCACPSLKRCPCICROT	592
OY	609	IKGTVRTFLS 618 	
Dd	593	IKGTVRTFLS 602	
RESULT	5		
O9UNH1	ID O9UNH1	PRELIMINARY:	PRT: 1140 AA.
AC	O9UNH1:		
DT	01-MAY-2000 (TREMBLrel. 13, Created)		
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)		
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)		
DE	API2-MLT FUSION PROTEIN.		
CN	API2-MLT.		
OS	Homo sapiens (human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
CC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=9272400; PubMed=10339464;		
RA	Dierlamme J., Beens M., Wlodarska I., Stefanova-Ouzounova M.,		
RA	Hendriks J.M., Hossfeld D.R., De Wolf-Peeters C., Hagemeijer A.,		
RA	Van den Bergh H., Marynen P.;		
RT	"The apoptosis inhibitor gene API2 and a novel 18q gene, MLT, are		
RT	recurrently rearranged in the t(11;18)(q21;q21)p6ssociated with		
RT	mucosa-associated lymphoid tissue lymphomas.";		
RL	Blood 93:3601-3609(1999).		
CC	-1 SIMILARITY: TO IMMUGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX		
CC	DOMAIN.		
DR	EMBL; AF123094; AAD46161.1; -.		
DR	HSP; Q13490; IOBH.		
DR	InterPro: IPR001370; BIR.		
DR	InterPro: IPR003576; Caspase-		
DR	InterPro: IPR001309; ICE_p20.		
DR	InterPro: IPR003558; IG_C2.		
DR	InterPro: IPR003600; IG_1like.		
DR	InterPro: IPR003006; IG_MHC.		
DR	Pfam: PF00653; BIR; 3.		
DR	Pfam: PF00047; IG; 2.		
DR	SMART; SM00238; BIR; 3.		
DR	SMART; SM00115; CASc; 1.		
DR	SMART; SM00408; ICc2; 1.		
DR	SMART; SM00410; IG_1like; 1.		
DR	PROSITE; PS01282; BIR_REPEAT_1; 3.		
DR	PROSITE; PS50143; BIR_REPEAT_2; 3.		
DR	PROSITE; PS50208; CASPASE_P20; 1.		
OQ	SEQUENCE 1140 AA: 128738 MW: 0C18DB90287C723E CRC64;		

```
Query Match      51.2%; Score 1678; DB 4; Length 1140;
Best Local Similarity 62.4%; Pred. No. 4,8e+10;
Matches 328; Conservative 61; Mismatches 105; Indels 32; Gaps 9;
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Db 2 NIVENSIFLUSMUSANFELKYLDSCELYEMSTYSTPEPAGVPSESLARAGFYTTGVN 61

QY 79 DKVACFCGGLMDNMWKLQSDSPLOKHKOIYBPCSPLONLVSA-SIGSTSKNTSP--MRNSF 135

Db 62 DKVACFCGGLMDNMWKLQSDSPLOKHKOIYBPCSPLONLVSA-SIGSTSKNTSP--MRNSF 120

QY 136 AHSLSPTLHSSLSFSGSYSLSPNPLNSRAVEDISSRPTNPVYSAMSTFEARFLTYHMP 195

Db 121 THSLPLPTENGSGYRGYSNSPNSPNVNSRANOQDSALMRSSYHCAMNENNRILITFYMP 180

QY 196 LTFUSPSELARAGFYIYGPGDVACFACGKLSMNEPKDAMSEHRRHPNCPLENSL- 254

Db 181 LTFUSPSELARAGFYIYGPGDVACFACGKLSMNEPKDAMSEHRRHPNCPLENSL- 240

QY 255 ETLFFSTNLSMOTHAAMRTFMPWSPVPQPOLASAGFYGYGRNDVYGCPCDDGLR 314

Db 241 DTSRTVSNLSMOTHAAMRTFMPWSPVPQPOLASAGFYGYGRNDVYGCPCDDGLR 300

QY 315 CMESGDDPWWVHAAMFPRCEFLIRBMKGGEFVDELQGRPHLEDLSTSDTGEENADP 374

Db 301 CMESGDDPWWVHAAMFPRCEFLIRBMKGGEFVDELQGRPHLEDLSTSDTGEENADP 360

QY 375 IIFHGPGSSSEDVAMNTPVYKSALENGENRDLVKOTVQSKILTTGENKTYVDIYSAL 434

Db 361 IIFHGPGSSSEDVAMNTPVYKSALENGENRDLVKOTVQSKILTTGENKTYVDIYSAL 420

QY 435 LNADEKKEEKEKQAEEMASDDLILPKNNMAL----FOOLTCVPLTDLMLKANYINK 490

Db 421 LNADEKKEEKEKQAEEMASDDLILPKNNMAL----FOOLTCVPLTDLMLKANYINK 471

QY 491 QEHDIIOKTOIPLQARELIDTILVKGNAANIFKNCLEKIDSTLY 536

Db 472 VOYQWFMKNKEIP-----NGWTSLLIF-NAVHVADAGFY 504

RESULT 6

Q9DDN2 PRELIMINARY; PRT; 324 AA.

AC Q9DDN2

DT 01-MAR-2001 (TREMblrel. 16, Created)

DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)

DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)

DE APOPTOSIS INHIBITOR CH-1APl (FRAGMENT).

OS Gallus gallus (Chicken).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

OC NCBI_TaxID=9031;

OX 11

RN SEQUENCE FROM N.A.

RP Pendleton C.N., Bargmann W.J., Varadarajan J., Rose H.R. Jr.; "The apoptosis inhibitor ch-1APl is a direct transcriptional target of v-Rel and c-Rel."

RT Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.

RL EMBL: AF311289; AAC42316.1; -.

DR InterPro: IPR001370; BIR.

DR Pfam: PF00653; BIR. 3.

DR SMART: SM00238; BIR. 3.

DR PROSITE: PS01282; BIR_REPEAT_1; 1.

DR PROSITE: PS0143; BIR_REPEAT_2; 3.

FT NON_TER 324 324

Q9 SEQUENCE 324 AA; 36567 MW; 5E2B89DEAE373F3 CRC64;

	Query Match	34.7%	Score 1138.5	DB 13	Length 324
	Best Local Similarity	63.4%	Pred. No. 1.2e-72		
	Matches	Conservative	49	Mismatches	55; Indels 15; Gaps 6;
OY	20 SIMEDSTILSDWNTSNKQ--KKMYDFSCGLRYRMSTYTFPAGVGVYSERSLARAGFYTTCV	77			
	::::: :: :	:			
Db	2 NIMDSPLSVYMKONHCGELKYDLSCELYRMTSETPFNVNVSERRLRARAGFYTTGV	61			
YY	78 NDVKYFCGCGMLDNMRLGDSPIDIKHKQLYPSCGFIGNLVSA-SLG-----SKN	127			

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Db 62 OQVKFCSCGLVLDNMQGDNAEMKHQVPSGCFVQNMLSLNLSTSHSAFSPVLVSN 121
      ||||| |||:||||: ||: |||||:|||||:||||: ||| ||
Qy 128 TSPMNSFAHSLPTLEHSLFSGSYSLSPNPLNSRAVEDISSRTNPSYAMSTPEAR 187
      || | :|||: | |||||: ||: |||||: ||: ||: |||||: ||
Db 122 LSPSLRSM--TLSPFEQVGFSSFSFPDDPYTTAAADLSHLKSLAHNSMSTEAR 179
      ||||| |||||:|||||: ||| |||||: |||||: |||||: |||||: ||
Qy 188 FLTYHMPPLTFLSPSELARAGFYITGPDRAVACGCGKLSNNEPKDAMSEHRRFPNC 247
      ||||| |||||:|||||: ||| |||||: |||||: |||||: |||||: ||
Db 180 LRTFHAMPLMFLSPTELAKAGLYLTGADKVACTCGGSLSNNEPKDAMSEHRRFPNC 239
      ||||| |||||:|||||: ||| |||||: |||||: |||||: |||||: ||
Qy 248 PLENSL-ETLRFSSISNLSMOTHAARMTEWMPSPVQPEOLASAGFYGYGRNDVVC 306
      ||||| |||||:|||||: |||||: |||||: |||||: |||||: |||||: ||
Db 240 PFVENLMRQPSFNVSNTTQTHERRFTFIMPTRIIPQPEOLADAGFYGYGRNDVVC 299
      ||||| |||||:|||||: |||||: |||||: |||||: |||||: |||||: ||
Qy 307 FCCDGLRCMESGDDPWVEMHAKWP 331
      ||||| |||||:|||||: |||||: |||||: |||||: |||||: |||||: ||
Db 300 FCCDGLRCMESGDDPWVEMHAKWP 324
      ||||| |||||:|||||: |||||: |||||: |||||: |||||: |||||: ||

RESULT 7
O88642 PRELIMINARY: PRT: 224 AA.
ID O88642
AC O88642:
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE INHIBITOR OF APOPTOSIS PROTEIN (FRAGMENT).
GN RIAP1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN (1)
RP SEQUENCE FROM N.A.
RA STRAIN=MISTAR; TISSUE=OVARY; CORPUS LUTEUM;
RA Bradley C.K., Lareu R.R., Dharmarajan A.M.;
RT "Cloning and characterization of an inhibitor of apoptosis protein
RT (IAP) in the rat corpus luteum."
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
RL EMBL: AF081503; AAC32497.1;
DR HSSP; Q13490; 108B.
DR InterPro; IPR001370; BIR.
DR Pfam; PF00653; BIR; 2.
DR SMART; SM00238; BIR; 2.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
FT NON_TER 1
FT NON_TER 224
FT SEQUENCE 224 AA; 25209 MW; 213A52534D5EB56A CRC64;

Query Match 28.9%; Score 945.5; DB 11; Length 224;
Best Local Similarity 74.9%; Pred. No. 3.1e-59;
Matches 173; Conservative 18; Mismatches 33; Indels 7; Gaps 3;
Qy 93 WKRGDPIKHKOLYPPSCSFIONLVASLSTGSKNTSPMNNFSAHSLPTLEHSLFSGS 152
      ||||| |||||:|||||: ||| |||||: |||||: |||||: |||||: ||
Db 1 WKRGDPIKHKOLYPPSCSFIONLVASLSTGSKNTSPMNNFSAHSLPTLEHSLFSGS 152
      ||||| |||||:|||||: ||| |||||: |||||: |||||: |||||: ||
Qy 153 YSLSLNPLNSRAVEDISSRTNPSYAMSTPEARLTLYHMPPLTFLSPSELARAGFYIT 212
      ||||| |||||:|||||: ||| |||||: |||||: |||||: |||||: ||
Db 55 HSLSLNPLNSRAVEDISSRTNPSYAMSTPEARLTLYHMPPLTFLSPSELARAGFYIT 113
      ||||| |||||:|||||: ||| |||||: |||||: |||||: |||||: ||
Qy 213 GPDRAVACGCGKLSNNEPKDAMSEHRRFPNCPLENSLFTLRFSISNLSMOTHAAR 272
      ||||| |||||:|||||: ||| |||||: |||||: |||||: |||||: ||
Db 114 GPDRAVACGCGKLSNNEPKDAMSEHRRFPNCPLENSLFTLRFSISNLSMOTHAAR 173
      ||||| |||||:|||||: ||| |||||: |||||: |||||: |||||: ||
Qy 273 MRFEMWPSVYQPEOLASAGFYGYGRNDVVCFCDDGLRCMESGDDPW 323
      ||||| |||||:|||||: ||| |||||: |||||: |||||: |||||: ||
Db 174 MRFEMWPSVYQPEOLASAGFYGYGRNDVVCFCDDGLRCMESGDDPW 224
      ||||| |||||:|||||: ||| |||||: |||||: |||||: |||||: ||

RESULT 8

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Q9E005
ID Q9E005 PRELIMINARY: PRT: 501 AA.
AC Q9E005:
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE INHIBITOR OF APOPTOSIS PROTEIN 3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN (1)
RP SEQUENCE FROM N.A.
RA STRAIN=MISTAR; TISSUE=OVARY;
RA Lareu R.R., Bradley C.K., Lacher M., Ellis R.R., Dharmarajan A.M.;
RT "Cloning, characterization and regulation of an inhibitor of apoptosis
RT protein in the rat corpus luteum."
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.
DR EMBL; AF304333; AAC41192.1;
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; ZnF_fing.
DR Pfam; PF00097; ZF-C3HC4; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 1.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
KW Zinc-finger.
SQ SEQUENCE 501 AA; 56548 MW; 0973FBF28B81C5A0 CRC64;

Query Match 27.4%; Score 898.5; DB 11; Length 501;
Best Local Similarity 33.4%; Pred. No. 1.8e-55;
Matches 204; Conservative 84; Mismatches 150; Indels 173; Gaps 15;
Qy 33 NSNMKMKDFCELYRMSTYSTEPAGVPSERSLAGEFYGYGVNDKYKFCFCGMLLDN 92
      ||||| |||||:|||||: ||| |||||: |||||: |||||: |||||: ||
Db 16 DTKNDE--EFVEERNRLKTFANPSSPVASATLABAGFLYTGEGDTVQCFCHAAVDR 72
      ||||| |||||:|||||: ||| |||||: |||||: |||||: |||||: ||
Qy 93 WKRGDPIKHKOLYPPSCSFIONLVASLSTGSKNTSP-----MNSFAHS 138
      ||||| |||||:|||||: ||| |||||: |||||: |||||: |||||: ||
Db 73 WQYGDVAAGRHRISPNCFFINGFFEN-GAT-OSTSPGICNGOYSENCVGNMPDYA 128
      ||||| |||||:|||||: ||| |||||: |||||: |||||: |||||: ||
Qy 139 LSPLEHSLFSGSYSLSPNPLNSRAVEDISSRTNPSYAMSTPEARLTLYHMPPL 197
      ||||| |||||:|||||: ||| |||||: |||||: |||||: |||||: ||
Db 129 ----LDRPSETHADYL-----LRTGVVDISDT-IYRNPAMCSEBARLKTPOAMPDYA 177
      ||||| |||||:|||||: ||| |||||: |||||: |||||: |||||: ||
Qy 198 FLSPSELARAGFYITGPDRAVACGCGKLSNNEPKDAMSEHRRFPNCPL 250
      ||||| |||||:|||||: ||| |||||: |||||: |||||: |||||: ||
Db 178 HUSPRELASAGLYTGIDVOYQCFCCGGLKNMPECDRAWSEHRRFPNCFFVLGRNVV 237
      ||||| |||||:|||||: ||| |||||: |||||: |||||: |||||: ||
Qy 251 -----ENSLFTLRFSISNLSMOTHAARMRTFMYWPSVYQPEOLASAGFYV 298
      ||||| |||||:|||||: ||| |||||: |||||: |||||: |||||: ||
Db 238 RSESGVSDRNPNPNTNSPR-----NPAAEYDARIYFGTMYLS--VNKEQLARAFYAL 291
      ||||| |||||:|||||: ||| |||||: |||||: |||||: |||||: ||
Qy 299 GRNDVVCFCFCGCGGKLRWESGDDPWVEMHAKWPCERCELIIMKGOBEVDLGGVPHLEQ 358
      ||||| |||||:|||||: ||| |||||: |||||: |||||: |||||: ||
Db 292 GEGDKVCFCHCGGLADMKPSDDPMEQHAKWYPCCKTLIDKEQGEYINNI-----HLTSS 346
      ||||| |||||:|||||: ||| |||||: |||||: |||||: |||||: ||
Qy 419 TTEGNYKYNDIVSALLNAEDKREEEKAEKAEEMADDSLIRKRNMLFQOULTVLP 478
      ||||| |||||:|||||: ||| |||||: |||||: |||||: |||||: ||
Db 398 TSGSNLSLEVLADIADVSKQKNSODE----- 424
      ||||| |||||:|||||: ||| |||||: |||||: |||||: |||||: ||
Qy 479 LDNLKANVINRQEDDIKQTOIPLQARBELDTILVKGAAANIFKNCIKETIDSTLYKN 538
      ||||| |||||:|||||: ||| |||||: |||||: |||||: |||||: ||
Db 425 -----SSQTSIQ----- 431
      ||||| |||||:|||||: ||| |||||: |||||: |||||: |||||: ||
Qy 539 LFVDKMKYIPTEDVSGLSLEQLRLQGEERTKVCMDKEVSVFIPCGLLVYCGECAPS 598
      ||||| |||||:|||||: ||| |||||: |||||: |||||: |||||: ||

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Db 432 -----KDISTEBQLRLQEBKLCIKMDRNIATVIFPCGHLVTKOCACAA 476
 OY 599 LKRCPIRGII 609
 Db 477 VDKCPMCTVI 487

RESULT 9
 O9EQ04 PRELIMINARY: PRT; 501 AA.
 ID O9EQ04:
 AC O9EQ04:
 DT 01-MAR-2001 (TReMBLrel. 16, Created)
 DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
 DE INHIBITOR OF APOPTOSIS PROTEIN 3.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 OX
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=WISTAR; TISSUE=OVARY;
 RA Lareu R.R., Bradley C.K., Lacher M., Frlis R.R., Dharmarajan A.M.;
 RT "Cloning, characterization and regulation of an inhibitor of apoptosis
 protein in the rat corpus luteum."
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.
 DR EMBL: AF304334; AACG1193.1; -.
 DR Interpro: IPR001370; BIR.
 DR Interpro: IPR001841; Znf_ring.
 DR Pfam: PF00653; BIR; 3.
 DR SMART: SM00238; zf-C3HC4; 1.
 DR SMART: SM00184; RING; 1.
 DR PROSITE: PS01282; BIR_REPEAT_1; 1.
 DR PROSITE: PS50143; BIR_REPEAT_2; 3.
 KW Zinc-finger.
 SQ SEQUENCE 501 AA; 56578 MW; 486369F2E0CCDC CRC64;

Query Match 27.4%; Score 898.5; DB 11; Length 501;
 Best Local Similarity 33.4%; Pred. No. 1.8e-55;
 Matches 204; Conservative 84; Mismatches 150; Indels 173; Gaps 15;
 OY 33 NSKKQMKATDSCELYRMSTSTFPAGVVSERSLARAGFYTGVDKVKFCGGLMDN 92
 Db 16 DTNKKDE--EFVEEFNRRLKTFANFPSSPVASSTLARAGFLYTGEQDVFCSCHAAVDR 72
 OY 93 WKLGDSPIQKHQKLYPSCSFIONLVASASLGSTSKNTSP-----MRNSFAHS 138
 Db 73 WQYGDASVGRHRRIRSPNCRFINCFYFEN-GAT-QSTSPGIONQVKSENCVGRNHFA-- 128
 OY 139 LSPLEHSLFSGSYSSLSPNLNSRAVEDISSRTNPTYSAMSTEARFLTYHMP-LT 197
 Db 129 ----LDRPSTHADYL-----LRTGOVVDISDT-IYPRNPAMCSSEARLKTQMPDYA 177
 OY 198 FLSPSELARAGFYIIGPGRVACFACGKLSNMEPKDAMDSEHRRHFPNCPFL----- 250
 Db 178 HLSPRELASAGLYTIDDOVQFCGCGKLNMEPCDRAHSEHRRHFPNCFVIGRNVN 237
 OY 251 -----ENSLLETIRFSISLSMOTHAARMRTFTWYPSVPVQPOLASAGFY 298
 Db 238 RSEGSVSSDRNPNSTNSPR---NPMAEYDARIIVFTGWLVS--VNKEQLARAGFYAL 291
 OY 299 GRNDVKKCPCCDGLRCWESGDDPVNEHAKWPRCEFLIRKGGEFVDELOGRYPHILRQ 358
 Db 292 GEBDKKCHCGGGLTDMKPSDEPWEQNAKYPCKKTLIDDEKGEYINNT-----HLTHS 346
 OY 359 LUSTDTTGENADPPIIHFGPESSSDAVAMNTPVYKSALEKGFNRDLVKOTVOSKIL 418
 Db 347 LGSVYVTRAEKT-----PSYTKKIDDTIFONPMVOEALRMGFNFKDKTKTMEKIQ 397

OY 419 TTGENYKTVNDIVSALLNADEREKEKQAEENASDLSLRKNRMALFOULTCVLP 478
 Db 398 TSGSNYLSLEVLIALDLVSAQKNSDSE----- 424
 OY 479 LDNLKKNVINKQEHDIKQKQIPIQARLIDTLVYGNAANIFKNCKLEIDSTLYKN 538
 Db 425 -----SSQTSIQ----- 431
 OY 539 LFDVKNMKYIPFEDVSGLSLEBQLRLQEBKTCYKMDKEVSVFTPCGHLVWCOCAPS 598
 Db 432 -----KDISTEBQLRLQEBKLCIKMDRNIATVIFPCGHLVTKOCACAA 476
 OY 599 LKRCPIRGII 609
 Db 477 VDKCPMCTVI 487

RESULT 10
 O9ESF0 PRELIMINARY: PRT; 496 AA.
 ID O9ESF0:
 AC O9ESF0:
 DT 01-MAR-2001 (TReMBLrel. 16, Created)
 DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
 DE INHIBITOR OF APOPTOSIS PROTEIN 3.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 OX
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Holcik M., Lefebvre C.A., Hicks K., Korneluk R.G.;
 RT "Cloning and Characterization of the Rat Homologs of the Inhibitor of
 Apoptosis Protein 1, 2, and 3 Genes."
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.
 DR EMBL: AF183429; AACG22969.1; -.
 DR Interpro: IPR001370; BIR.
 DR Interpro: IPR001841; Znf_ring.
 DR Pfam: PF00653; BIR; 3.
 DR Pfam: PF00097; zf-C3HC4; 1.
 DR SMART: SM00238; BIR; 3.
 DR SMART: SM00184; RING; 1.
 DR PROSITE: PS01282; BIR_REPEAT_1; 1.
 DR PROSITE: PS50143; BIR_REPEAT_2; 3.
 KW Zinc-finger.
 SQ SEQUENCE 496 AA; 56117 MW; 9BEF142AAEC5B798 CRC64;

Query Match 27.4%; Score 896.5; DB 11; Length 496;
 Best Local Similarity 33.1%; Pred. No. 2.5e-55;
 Matches 205; Conservative 86; Mismatches 155; Indels 173; Gaps 15;
 OY 33 NSKKQMKATDSCELYRMSTSTFPAGVVSERSLARAGFYTGVDKVKFCGGLMDN 92
 Db 16 DTNKKDE--EFVEEFNRRLKTFANFPSSPVASSTLARAGFLYTGEQDVFCSCHAAVDR 72
 OY 93 WKLGDSPIQKHQKLYPSCSFIONLVASASLGSTSKNTSP-----MRNSFAHS 138
 Db 73 WQYGDASVGRHRRIRSPNCRFINCFYFEN-GAT-QSTSPGIONQVKSENCVGRNHFA-- 128
 OY 139 LSPLEHSLFSGSYSSLSPNLNSRAVEDISSRTNPTYSAMSTEARFLTYHMP-LT 197
 Db 129 ----LDRPSTHADYL-----LRTGOVVDISDT-IYPRNPAMCSSEARLKTQMPDYA 177
 OY 198 FLSPSELARAGFYIIGPGRVACFACGKLSNMEPKDAMDSEHRRHFPNCPFL----- 250
 Db 178 HLSPRELASAGLYTIDDOVQFCGCGKLNMEPCDRAHSEHRRHFPNCFVIGRNVN 237
 OY 251 -----ENSLLETIRFSISLSMOTHAARMRTFTWYPSVPVQPOLASAGFY 298
 Db 238 RSEGSVSSDRNPNSTNSPR---NPMAEYDARIIVFTGWLVS--VNKEQLARAGFYAL 291

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QY 299 GANDVYKFCDDGRLRCWESGDDPWVBAHAPRCPCELLIRMGQEFVDEIGRYPHLEO 358
DB 292 GEGDVYKFCGCGGLTDMKPESEDEPQAHAKWPGCYLLDEKGOEYINNI-----HLTHS 346
QY 359 ILSTDITGEENADPPIIHFGPESSEDVAMNPFVKSALFMGFNRDLVKOTVOSKIL 418
DB 347 LGESEVYRRAEKT-----PSVTKKIDDTIFONPMVOEALIRMGNFPRDIKKIMEKLO 397
QY 419 TTGENYKTVNDIVSALLNAEDEREKEKQADEMASDSLIRKNRMALFOQLTCVLP 478
DB 398 TSGSNYLSLEVLIADIVSAOKNSQDE----- 424
QY 479 LDNLKANVINKQEHDIKQKTOPLQARBLIDTILVKGMAANIPKNCLEIDSTLYKN 538
DB 425 -----SSQTSILO----- 431
QY 539 LEVDKNMKYIPTEVSGLSLEBQLRLQERTCKVCMKEVSVYRIPCGHLVVOCEKAPS 598
DB 432 -----KDISTEEDQLRLQEBKLCCKICMDRIALVFPVCGHLVTCQCAEA 476
QY 599 LRKCPICRGITKGVTRPL 617
DB 477 VDKCPMCTCTVITFKQIKFM 495

RESULT 11
Q9IA69 PRELIMINARY; PRT; 197 AA.
AC Q9IA69;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE INHIBITOR OF APOPTOSIS 1 (FRAGMENT).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauaria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRED FAYOUMI; TISSUE=SPLEEN;
RA Zhou H., Lamont S.J.;
RT "Genetic variation among chicken lines and mammalian species in
RT specific genes.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF221083; AAF35320.1; -.
DR InterPro; IPR001370; BIR.
DR Pfam; PF00653; BIR; 2.
DR SMART; SM00238; BIR; 2.
DR PROSITE; PS01282; BIR_REPEAT_1; 2.
DR PROSITE; PS50143; BIR_REPEAT_2; 2.
FT NON_TER 1
FT NON_TER 197
FT SEQUENCE 197 AA; 22602 MW; D7923DABCF623E1A CRC64;

Query Match 24.5%; Score 801.5; DB 13; Length 197;
Best Local Similarity 68.4%; Pred. No. 3.9e+49;
Matches 134; Conservative 33; Mismatches 28; Indels 1; Gaps 1;

QY 155 SLSPNPLNSRAVEDISSRTNPYSAMSTEARFLTYHMPPLFLSPSELARAGFYIGP 214
DB 1 SPQDPVYTTBRAEDLSHRSKLHNPMSSTEARLRTHFAPLMLFSLPTELAKGLYLYCT 61
QY 215 GDRVACFCAGCGKLSNWEKDDAMSEHRRHPNCPLENSL-ETLRFISINLSMOTHAARM 273
DB 62 ADVACFCFCGGLSNWEKDDAMSEHRRHPNCPLENSL-ETLRFISINLSMOTHAARM 121
QY 274 RRFMYWPSVVPQPOLASAGFYVYGRNDVKFCFCGGLRCWESGDDPWVEHAKWPRC 333
DB 122 KTFINMPTRIPVQPOLADAGFYVYGRNDVKFCFCGGLRCWESGDDPWIEHAKWPRC 181
QY 334 EFLIRMKQGEFVDEIG 349

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DB 182 EYLIRVKGGEFVSQV 197

RESULT 12
Q9IA70 PRELIMINARY; PRT; 195 AA.
AC Q9IA70;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE INHIBITOR OF APOPTOSIS 1 (FRAGMENT).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauaria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRED LEKHORN; TISSUE=SPLEEN;
RA Zhou H., Lamont S.J.;
RT "Genetic variation among chicken lines and mammalian species in
RT specific genes.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF221082; AAF35319.1; -.
DR InterPro; IPR001370; BIR.
DR Pfam; PF00653; BIR; 2.
DR SMART; SM00238; BIR; 2.
DR PROSITE; PS01282; BIR_REPEAT_1; 2.
DR PROSITE; PS50143; BIR_REPEAT_2; 2.
FT NON_TER 1
FT NON_TER 195
FT SEQUENCE 195 AA; 22347 MW; 9C39BFA755E24E48 CRC64;

Query Match 24.3%; Score 796.5; DB 13; Length 195;
Best Local Similarity 68.2%; Pred. No. 8.6e+49;
Matches 133; Conservative 33; Mismatches 28; Indels 1; Gaps 1;

QY 155 SLSPNPLNSRAVEDISSRTNPYSAMSTEARFLTYHMPPLFLSPSELARAGFYIGP 214
DB 1 SPQDPVYTTBRAEDLSHRSKLHNPMSSTEARLRTHFAPLMLFSLPTELAKGLYLYCT 60
QY 215 GDRVACFCAGCGKLSNWEKDDAMSEHRRHPNCPLENSL-ETLRFISINLSMOTHAARM 273
DB 61 ADVACFCFCGGLSNWEKDDAMSEHRRHPNCPLENSL-ETLRFISINLSMOTHAARM 120
QY 274 RRFMYWPSVVPQPOLASAGFYVYGRNDVKFCFCGGLRCWESGDDPWVEHAKWPRC 333
DB 121 KTFINMPTRIPVQPOLADAGFYVYGRNDVKFCFCGGLRCWESGDDPWIEHAKWPRC 180
QY 334 EFLIRMKQGEFVDEI 348
DB 181 EYLIRVKGGEFVSQV 195

RESULT 13
Q9R015 PRELIMINARY; PRT; 597 AA.
AC Q9R015;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE NEURONAL APOPTOSIS INHIBITORY PROTEIN.
GN BIRC6 OR NAI1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9431676; PubMed=10501978;
Huang S., Scharf J.M., Growney J.D., Endrizzi M.G., Dietrich W.F.;

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RT "The mouse Naip gene cluster on Chromosome 13 encodes several distinct functional transcripts.";
 RL Mamm. Genome 10:1032-1035(1999).
 DR EMBL: AF135493; AAD56765.1; -.
 DR HSSP: Q13490; 1QBH.
 DR MGD: MGI:1296220; Bircle.
 DR InterPro: IPR001370; BIR.
 DR Pfam: PF00653; BIR; 3.
 DR SMART: SM00238; BIR; 3.
 DR PROSITE: PS01282; BIR_REPEAT_1; UNKNOWN_2.
 DR PROSITE: PS0143; BIR_REPEAT_2; 3.
 DR SEQUENCE 597 AA; 68322 MW; 4042E36E51A7F9A0 CRC64;

Query Match 15.18; Score 494; DB 11; Length 597;
 Best Local Similarity 26.38; Pred. No. 8.1e-77;
 Matches 163; Conservative 78; Mismatches 197; Indels 182; Gaps 23;

38 KKKYDFSC-----LYRMSTSTPPAGVPSERSIARAGFYTGVDNKKVCCGGLML 90
 2 KKKKGFNSQMSEAKRLKTFETDTFTFSWTP---QEMAAAGFYHTGVRGLGVCFCGLL 58
 91 DNMLGDSPIQKHQOLYPCSFIONLVASLSTKNTSPMNSFAHLSPTLEHSLFS 150
 59 FGNSLRKLPERRHKKLRPECEFLQGDVGNIGK-----YDIRKVRPEKMLG 105
 151 GSYSLSPNPLNSRAVEDISSRTNPYSAMSTFEARFLTYHMMPLTF--LSPSELARAG 208
 106 G-----KARHE-----DEALSEFEDMPYRAGTSPRVLSAAG 139
 209 FYIYIGCDRVACFACGCGKLSMWEKDDAMSEHRRHPNCPLEN--SLETLRFISINLSM 266
 140 FVFTGRDVTQVCFSCGSGSLGNMEGDDPMKEHAKMFKCEFLQSKKSSEELIAYISYGC 199
 267 QTHAA-----BMRFFMVPSSVPYQPEGLASAGPY 296
 200 FVHTGGEHFVSWVRRELPMVSAVCSNDVSFANEELRNDRMKDPQESPVGEALVAGGF 259
 297 YVGRNDVYKFCPCDGLRCWESGDDPVWEHAKWPRCEFLIRNKGQ-EFYDELIGRYPHL 355
 260 YGKKDIYVNCFCGCGCLTEKMAEGDDPMEDHIFKPECEVLTQLTSSAEVITLQSOY--- 316
 356 LQGLLSTDTTGEEN-ADPPIIHFHFGPSSSEDVAMNTFVYVSA-----LEMGF 404
 317 --ALPEATETRESNMGDAVAH-----STVYKVFIONFPLAHVFLKCFD 360
 405 --NRDLVYKOTVOS-----KILTTGENTKV-----NDIVSALLNADEK--REEEKEK 448
 361 LENCESLMAVILASCKKLEIFSGRCPEAMTFVNLDPFVSLKILNLKDOQFDPKETSXK 420
 449 OAEEMASDQLSIKRNKRALQOULTCVPLIDNL--KAVINIKOEHDILKOKTQIP--- 503
 421 FQALGSS-----LRNLEELLVPTGGIHQVAKLIYKQCLDLCLAR 460
 504 -LQARELI--DTILYKNAAMNIFKNCLKEIDSTL-----YKNLFYDNKNKYIPTED 552
 461 VLFPHDILDDDSVEIILAAATSGCFQKLENDISMNKITEGVRNPF----- 508
 553 VSGLSLEQDLRLQLEFRCK 572
 509 ---QALDMLPVLDLNLICR 524

RESULT 14
 OGVUX5 PRELIMINARY; PRT; 438 AA.
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE TH GENE PRODUCT.
 GN TH OR CG12284.
 OS Drosophila melanogaster (fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pelecygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_Taxid:7227;
 RN [1]
 RE SEQUENCE FROM N.A.
 RC STRAIN-BEKKLEY;
 RX MEDLINE-20196006; PubMed-10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.C., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer V.R.G., Champe M., Pfeiffer B.D.,
 RA Van K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Bailliv R.M., Basu A., Bendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bereman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
 RA Burris K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.P., Dew I., Dietz S.M.,
 RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.G., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mlshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclob J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Sytaekas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).
 CC -1; SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.
 DR EMBL: AF003528; AAG22319.1; -.
 DR HSSP: Q13490; 1QBH.
 DR FLYbase: FBgn0003691; th.
 DR InterPro: IPR001370; BIR.
 DR InterPro: IPR001841; ZnF_rlng.
 DR Pfam: PF00653; BIR; 2.
 DR Pfam: PF00097; ZF-C3HC4; 1.
 DR SMART: SM00238; BIR; 2.
 DR SMART: SM00184; RING; 1.
 DR PROSITE: PS01282; BIR_REPEAT_1; 2.
 DR PROSITE: PS0143; BIR_REPEAT_2; 2.
 DR Zinc-finger.
 SO SEQUENCE 438 AA; 48038 MW; 24CA8BC13F5DDEF31 CRC64;

Query Match 15.0%; Score 490; DB 5; Length 438;
 Best Local Similarity 22.8%; Pred. No. 1e-26;
 Matches 127; Conservative 61; Mismatches 128; Indels 242; Gaps 11;
 162 NSRAVE-----DISSRTNPYSAMSTFEARFLTYHMMPLTFLSPSELARAGFYGGPDR 217
 22 NTNATQTFKNNKTRND--LNRDETRLKTFEDWPLDWLKDRLQVGTGVTNHADK 77
 218 VACFACGKLSMWEKDDAMSEHRRHPNCPF-----LENSETLRFST- 261
 78 VKCFGVEIGCMQEDQPPVPEHOKRSPNCPILLRRRTNNVFINAEALDRILPISYDIC 137


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QY 262 -----SNLSMOTHA----- 270
DB 138 GANDSTLMBREHAYAEVYIPMSOLIOSIGNAVNAAGSVTGAAPQPRVTAHTASTATQ 197
QY 271 -----ARMTEWPPSSVPQPEOLASAGFYVGR 300
DB 198 ATGDVQPETCRPSAASGNFYQYPEVAIETARLRTFEAMPRLKQKPHQLAAGFEFTYGV 257
QY 301 NDDVYCFCCDGLRCWESSGDDPWVEHAKMPRCEFLIRKGOEFVDEIOGRPHILEOLL 360
DB 258 GDRKRCSCGGGLMDMDNDDEPWOHALMLOCRFVKILKGOLYIDY----- 305
QY 361 STSDTTGEEADPPIIHFGPGESSSEDAVMNTPVYKSALEMGFNDLYKQTVOSKILTT 420
DB 306 -----AAKPVLAEKEEKESSIGV----- 324
QY 421 GENKTVNDIYSALLNAEDEKREBEKKOEEMASDLSLRKRNALFOQLTCVLPILD 480
DB 325 -----AAVASTQASEEEOQTSLSSEAVSGDVA-----PSVAP--- 356
QY 481 MLKANVINKEHDIKOKTOIPLQARELIDTLVKNNAANIFKNCKLEIDSTLYKNLF 540
DB 357 -----TATATRLT-----NKI 366
QY 541 VDKNMKIYPTEDVSGLSLEOLRLQBERCKYCMDEKSVVFIQGHILVCOECAPSRLR 600
DB 367 VETAAVATPSTNSSGST-----SIPEKCLKICYGAEYNTAFLPCGHVAVCAKCASSVT 420
QY 601 KCPICRGITKGTVPFLS 618
DB 421 KCPICRKRPFTVMRYES 438

RESULT 15
QYINL8 PRELIMINARY; PRT: 281 AA.
AC Q9YNL8:
DT 01-MAY-1999 (TREMblrel. 10, Created)
DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE IAP PROTEIN.
GN IAP.
OS Choristoneura fumiferana nuclear polyhedrosis virus (CFMNPV).
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxID=10448;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IRELAND;
RA Lauzon H., Ailif B.M., Ladd T., Palli R.;
RT "CFMNPV IAP gene."
RL Submitted (DEC-1996) to the EMBL/GenBank/DDbj databases.
CC -1- SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.
DR EMBL: U82510; AAD00537.1; -.
DR HSP; Q13490.10BH.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001841; ZnF_fing.
DR Pfam: PF00653; BIR; 2.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00238; BIR; 2.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01267; BIR_REPEAT_1; UNKNOWN_1.
DR PROSITE: PS50143; BIR_REPEAT_2; 2.
DR Zinc-finger.
KW
SQ SEQUENCE 281 AA; 32090 MW; B2D9BEBA359F105E CRC64;

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Query Match 14.8%; Score 486; DB 12; Length 281;

Best Local Similarity 24.5%; Pred. No. 11e-26;

Matches 112; Conservative 43; Mismatches 89; Indels 214; Gaps 6;

QY 181 MSTEERARLYHMPLTFLSPSELARAGFYIGPGRVACFACGGKLSNWEPRKDMASEH 240

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DB 14 MEDENARLATYNNWTVVEEMSPROMAANGFYLLGSDGVRCAFCKVNLKREAGDOPAROH 73
QY 241 RHFPNCPPLNSLETL-----RFSISNL-----SMOTHAARMKTEFY 278
DB 74 OKWAPDCPFLRRSGATLSAPOERAGLHAPOEREAATNOLPSPPAHPRKVAIEAARLRTETE 133
QY 279 WPSVYVPOEOLASAGFYVGRNDVQCFCCDGLRCWESSGDDPWVEHAKMPRCEFLIR 338
DB 134 WFRGLKORPEKLAEGFYTGSRDKVCKFCDDGLMDQDDDEPWOHALMFGRCAYVLL 193
QY 339 MKGOEFVDEIOGRPHILEOLLSTSDTTGEEADPPIIHFGPGESSSEDAVMNTPVYKS 398
DB 194 VKGRDYQKV-----VTESCAIRDTT----- 214
QY 399 ALEMGFNDLYKQTVOSKILTTGENYKTVNDIYSALLNAEDEKREBEKKOEEMASDLS 458
DB 215 -----KKOVAKHTV----- 223
QY 459 SLIRKRNALFOQLTCVLPILDMLKANVINKEHDIKOKTOIPLQARELIDTLVKNGN 518
DB 224 ----- 223
QY 519 AANIFKNCKLEIDSTLYKNLFVDKNMKIYPTEDVSGLSLEOLRLQBERCKYCMDEK 578
DB 224 -----YEP-----NLPDEKCLKICTYDE 241
QY 579 VSVYFIQGHILVCOECAPSRLKCPICRGITKGTVPFL 616
DB 242 KIVCFVPCGHVAVCAKCASSLTNCPICRVYETAVRMY 279

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Search completed: January 7, 2002, 16:03:52
Job time: 1411 sec

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